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<120> MKK7y1 Nucleic Acids and Polypeptides

<130> PC018226A

<140> PCT US 00/000000

<141> 2003-08-18

<150> 60/425,581

<151> 2002-11-12

<160> 23

<170> PatentIn version 3.1

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Met Ala Ala Ser Ser Leu Glu Gln Lys Leu Ser Arg Leu Glu Ala Lys
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
          20          25          30

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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
          35          40          45

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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65          70          75          80

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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
          85          90          95

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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
          100          105          110

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Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
          115          120          125

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Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
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Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
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Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
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Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
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Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
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Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Ser Lys
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Ala Lys Thr Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
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Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
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Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
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Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
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Met Ala Ala Ser Ser Leu Glu Gln Lys Leu Ser Arg Leu Glu Ala Lys
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
          20          25          30

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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
          35          40          45

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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
          50          55          60

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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65          70          75          80

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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
          85          90          95

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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
          100          105          110

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Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
          115          120          125

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Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
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Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
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Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
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Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
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Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
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His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
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Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Asp Lys
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Ala Lys Asp Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
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Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
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Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
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Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro
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Phe Phe Arg
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
145 150 155 160

Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Asp Lys
275 280 285

Ala Lys Glu Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu

385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
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Phe Phe Arg
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
          20          25          30

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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
          35          40          45

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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
          50          55          60

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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65          70          75          80

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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
          85          90          95

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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
          100          105          110

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Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
          115          120          125

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Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
          130          135          140

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Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
145          150          155          160

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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn

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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val	195	200	205		
Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys	210	215	220		
Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val	225	230	235	240	
Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile	245	250	255		
His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln	260	265	270		
Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Glu Lys	275	280	285		
Ala Lys Asp Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg	290	295	300		
Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp	305	310	315	320	
Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe	325	330	335		
Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu	340	345	350		
Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp	355	360	365		
Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg	370	375	380		
Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu	385	390	395	400	

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
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Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro
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Phe Phe Arg
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Met Ala Ala Ser Ser Leu Glu Gln Lys Leu Ser Arg Leu Glu Ala Lys
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
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Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
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Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
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Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Glu Lys
275 280 285

Ala Lys Glu Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro
420 425 430

Phe Phe Arg
435

<210> 11
<211> 1308
<212> DNA
<213> Mus musculus

<400> 11
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cccattattg tgatcactct aagccctgct cctgccccgt cccagcgagc agccctgcaa 180
ctcccactgg ccaacgatgg gggcagccgc tcaccatcct cagagagctc cccacagcac 240
cctacacccc ccacccggcc ccgccacatg ctggggctcc catcaacctt gttcacaccg 300
cgcagtatgg agagcatcga gattgaccag aagctgcagg agatcatgaa gcagacaggg 360
tacctgacta tcggggggcca gcgttatcag gcagaaatca atgacttgga gaacttgggt 420
gagatgggca gtggtacctg tggtcagggt tggaagatgc gggtccggaa gacaggccac 480
atcattgctg ttaagcaa at gcggcgctct gggaacaagg aagagaataa gcgcattttg 540
atggacctgg atgtagtact caagagccat gactgccctt acatcggttca gtgctttggc 600
accttcatca ccaacacaga cgtcttttatt gccatggagc tcatggggcac atgtgcagag 660
aagctgaaga aacgaatgca gggccccatt ccagagcgaa tcctgggcaa gatgactgtg 720
gcgatttgta aagcactgta ctatctgaag gagaagcatg gcgtcatcca tcgcgatgtc 780
aaacctcca acatcctgct agatgagcgg ggccagatca agctctgtga ctttggcatc 840
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gctcccgagc gcatcgacct tccagatccc accaagcctg actatgacat ccgagctgat 960
gtgtggagcc tgggcatctc actggtggag ctggcaacag gacagttccc ctataagaac 1020
tgcaagacgg actttgaggt cctcaccaaa gtcctacagg aagagcccc actcctgcct 1080
ggtcacatgg gcttctcagg ggacttcag tcatttgtca aagactgcct tactaaagat 1140

cacaggaaga gaccaaagta taataagcta cttgaacaca gcttcatcaa gcactatgag 1200
atactcgagg tggatgtcgc gtcctgggtt aaggatgtca tggcgaagac cgagtcccca 1260
aggactagtg gagtccctgag tcagcaccat ctgcccttct tcaggtag 1308

<210> 12
<211> 435
<212> PRT
<213> Mus musculus

<400> 12

Met Ala Ala Ser Ser Leu Glu Gln Lys Leu Ser Arg Leu Glu Ala Lys
1 5 10 15

Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
20 25 30

Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65 70 75 80

Pro Thr Pro Pro Thr Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Leu Thr Ile Gly Gly Gln Arg
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
145 150 155 160

Ile Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Ser Lys
275 280 285

Ala Lys Thr Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys His Tyr Glu
385 390 395 400

Ile Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln His His Leu Pro
420 425 430

Phe Phe Arg
435

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
atggcggcgt cctccctgga acagaag 27

<210> 14
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
ggcaggagca gggcttagag tgatcacaat aatgg 35

<210> 15
<211> 156
<212> DNA
<213> Human

<400> 15
atggcggcgt cctccctgga acagaagctg tcccgctgg aagcaaagct gaagcaggag 60

aaccgggagg cccggcggag gatcgacctc aacctggata tcagccccca gcggcccagg 120

cccattattg tgatcactct aagccctgct cctgcc 156

<210> 16
<211> 48
<212> DNA
<213> Human

<400> 16
attattgtga tcaactctaag ccctgctcct gccccgtccc aacgagca 48

<210> 17
 <211> 435
 <212> PRT
 <213> Human

<220>
 <221> MISC_FEATURE
 <222> (291)..(291)
 <223> Xaa is Aspartic Acid, Glutamic Acid, or Threonine

<220>
 <221> MISC_FEATURE
 <222> (293)..(293)
 <223> Xaa is Aspartic Acid, Glutamic Acid, or Serine

<220>
 <221> MISC_FEATURE
 <222> (287)..(287)
 <223> Xaa is Aspartic Acid, Glutamic Acid, or Serine

<400> 17

Met Ala Ala Ser Ser Leu Glu Gln Lys Leu Ser Arg Leu Glu Ala Lys
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
 20 25 30

Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
 35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
 50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
 65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
 85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
 100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
 115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
145 150 155 160

Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Xaa Lys
275 280 285

Ala Lys Xaa Arg Xaa Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro
420 425 430

Phe Phe Arg
435

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gggaaacata tggcggcgtc ctcc 24

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
ggatccctac ctgaagaagg gcaggtgg 28

<210> 20
<211> 1260
<212> DNA
<213> Human

<400> 20
atggcggcgt cctccctgga acagaagctg tcccgcctgg aagcaaagct gaagcaggag 60
aaccgggagg cccggcggag gatcgacctc aacctggata tcagcccccga gcggccccagg 120

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cccaccctgc agctcccgt ggccaacgat gggggcagcc gctcgccatc ctcagagagc 180
tccccgcagc accccacgcc ccccgcccgg ccccgccaca tgctggggct cccgtcaacc 240
ctgttcacac cccgcagcat ggagagcatt gagattgacc agaagctgca ggagatcatg 300
aagcagacgg gctacctgac catcgggggc cagcgctacc aggcagaaat caacgacctg 360
gagaacttgg gcgagatggg cagcggcacc tgcggccagg tgtggaagat gcgcttccgg 420
aagaccggcc acgtcattgc cgtaagcaa atgcggcgct ccgggaacaa ggaggagaac 480
aagcgcatcc tcatggacct ggatgtggtg ctgaagagcc acgactgccc ctacatcgtg 540
cagtgccttg ggacgttcat caccaacacg gacgtcttca tcgccatgga gctcatgggc 600
acctgcgctg agaagctcaa gaagcggatg cagggcccca tccccgagcg cattctgggc 660
aagatgacag tggcgattgt gaaggcgctg tactacctga aggagaagca cgggtgcatc 720
caccgcgacg tcaagccctc caacatcctg ctggacgagc ggggccagat caagttctgc 780
gacttcggca tcagcggccg cctggtggac tccaaagcca agacgcggag cgccggctgt 840
gccgcctaca tggcacccga gcgcattgac ccccagacc ccaccaagcc ggactatgac 900
atccggggcg acgtatggag cctgggcatc tcgctggtgg agctggcaac aggacagttt 960
ccctacaaga actgcaagac ggactttgag gtcctcacca aagtcctaca ggaagagccc 1020
ccgcttctgc cggacacat gggcttctcg ggggacttcc agtccttcgt caaagactgc 1080
cttactaaag atcacaggaa gagaccaaag tataataagc tacttgaaca cagcttcatc 1140
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<210> 21
<211> 13
<212> PRT
<213> Artificial Sequence

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<220>
<223> Tag

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<400> 21

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Met Gly Ser Ser His His His His His His Ser Ser Gly
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<210> 22
<211> 1308
<212> DNA

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<213> Human

<400> 22

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aaccgggagg cccggcggag gatcgacctc aacctggata tcagccccca gcggcccagg      120
cccattattg tgatcactct aagccctgct cctgccccgt cccaacgagc agccctgcag      180
ctcccgtctg ccaacgatgg gggcagccgc tcgccatcct cagagagctc cccgcagcac      240
cccacgcccc ccgcccggcc ccgccacatg ctgggggtcc cgtcaaccct gttcacaccc      300
cgcagcatgg agagcattga gattgaccag aagctgcagg agatcatgaa gcagacgggc      360
tacccgacca tcggggggcca gcgctaccag gcagaaatca acgacctgga gaacttgggc      420
gagatgggca gcggcacctg cggccagggt tggaagatgc gcttccggaa gaccggccac      480
gtcattgccg ttaagcaaat gcggcgctcc gggaacaagg aggagaacaa gcgcatcctc      540
atggacctgg atgtggtgct gaagagccac gactgcccct acatcgtgca gtgctttggg      600
acgttcatca ccaacacgga cgtcttcacg gccatggagc tcatgggcac ctgcgctgag      660
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gcgattgtga aggcgctgta ctacctgaaa gagaagcacg gtgtcatcca ccgcgacgtc      780
aagccctcca acatcctgct ggacgagcgg ggccagatca agctctgcga cttcggcatc      840
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gcacccgagc gcattgacct ccagacccc accaagccgg actatgacat ccggggccgac      960
gtatggagcc tgggcatctc gttggtggag ctggcaacag gacagtttcc ctacaagaac     1020
tgcaagacgg actttgaggt cctcaccaaa gtcctacagg aagagcccc gcttctgccc     1080
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cacaggaaga gaccaaagta taataagcta cttgaacaca gttcatcaa gcgctacgag     1200
acgctggagg tggacgtggc gtctgtgttc aaggatgtca tggcgaagac tgagtcaccg     1260
cggactagcg gcgtcctgag ccagccccac ctgcccttct tcaggtag                       1308

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<210> 23

<211> 435

<212> PRT

<213> Human

<400> 23

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Met Ala Ala Ser Ser Leu Glu Gln Lys Leu Ser Arg Leu Glu Ala Lys
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
20 25 30

Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
145 150 155 160

Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Glu Lys
275 280 285

Ala Lys Glu Arg Glu Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro
420 425 430

Phe Phe Arg
435